



SEQUENCE LISTING

RECEIVED

JUN 14 2002

TECH CENTER 1600/2900

<110> Kaufman, Randal J.
Tirasophon, Witoon
Welihinda, Ajith A.

<120> Irelp, A NOVEL MAMMALIAN PROTEIN AND GENE ENCODING SAME

<130> UMV-1584

<140> US 09/357,273

<141> 1999-07-20

<150> US 60/093,526

<151> 1998-07-21

<160> 13

<170> PatentIn Ver. 2.0

<210> 1

<211> 3629

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (97)..(3027)

<400> 1

ccggctcgac ggctcgggtca ccgcctcgct gtcgtcgcgg cgcccccggc cgtcctctgt 60

ccgtaccgcc cccggagcca gggccgagtc ctcgcc atg ccg gcc cgg cgg ctg 114
Met Pro Ala Arg Arg Leu
1 5

ctg ctg ctg ctg acg ctg ctg ctg ccc ggc ctc ggg att ttt gga agt 162
Leu Leu Leu Leu Thr Leu Leu Leu Pro Gly Leu Gly Ile Phe Gly Ser
10 15 20

acc agc aca gtg acg ctt cct gaa acc ttg ttg ttt gtg tca acg ctg 210
Thr Ser Thr Val Thr Leu Pro Glu Thr Leu Leu Phe Val Ser Thr Leu
25 30 35

gat gga agt ttg cat gct gtc agc aag agg aca ggc tca atc aaa tgg 258
Asp Gly Ser Leu His Ala Val Ser Lys Arg Thr Gly Ser Ile Lys Trp
40 45 50

act tta aaa gaa gat cca gtc ctg cag gtc cca aca cat gtg gaa gag 306
Thr Leu Lys Glu Asp Pro Val Leu Gln Val Pro Thr His Val Glu Glu
55 60 65 70

cct gcc ttt ctc cca gat cct aat gat ggc agc ctg tat acg ctt gga 354
Pro Ala Phe Leu Pro Asp Pro Asn Asp Gly Ser Leu Tyr Thr Leu Gly
75 80 85

agc aag aat aat gaa ggc ctg acg aaa ctt cct ttt acc atc cca gaa 402
Ser Lys Asn Asn Glu Gly Leu Thr Lys Leu Pro Phe Thr Ile Pro Glu
90 95 100

ttg gtg cag gca tcc cca tgc cga agt tca gat gga atc ctc tac atg 450

COPY OF PAPERS
ORIGINALLY FILED

Leu Val Gln Ala Ser Pro Cys Arg Ser Ser Asp Gly Ile Leu Tyr Met	
105 110 115	
ggt aaa aag cag gac atc tgg tat gtt att gac ctc ctg acc gga gag	498
Gly Lys Lys Gln Asp Ile Trp Tyr Val Ile Asp Leu Leu Thr Gly Glu	
120 125 130	
aag cag cag act ttg tca tgc gcc ttt gca gat agt ctc tgc cca tca	546
Lys Gln Gln Thr Leu Ser Ser Ala Phe Ala Asp Ser Leu Cys Pro Ser	
135 140 145 150	
acc tct ctt ctg tat ctt ggg cga aca gaa tac acc atc acc atg tac	594
Thr Ser Leu Leu Tyr Leu Gly Arg Thr Glu Tyr Thr Ile Thr Met Tyr	
155 160 165	
gac acc aaa acc cga gag ctc cgg tgg aat gcc acc tac ttt gac tat	642
Asp Thr Lys Thr Arg Glu Leu Arg Trp Asn Ala Thr Tyr Phe Asp Tyr	
170 175 180	
gcg gcc tca ctg cct gag gac gaa ggg gac tac aag atg tcc cac ttt	690
Ala Ala Ser Leu Pro Glu Asp Glu Gly Asp Tyr Lys Met Ser His Phe	
185 190 195	
gtg tcc aat ggt gat ggg ctg gtg gtg act gtg gac agt gaa tct ggg	738
Val Ser Asn Gly Asp Gly Leu Val Val Thr Val Asp Ser Glu Ser Gly	
200 205 210	
gac gtc ctg tgg atc caa aac tac gcc tcc cct gtg gtg gcc ttt tat	786
Asp Val Leu Trp Ile Gln Asn Tyr Ala Ser Pro Val Val Ala Phe Tyr	
215 220 225 230	
gtc tgg cag cgg gag ggt ctg agg aag gtg atg cac atc aat gtc gct	834
Val Trp Gln Arg Glu Gly Leu Arg Lys Val Met His Ile Asn Val Ala	
235 240 245	
gtg gag acc ctg cgc tat ctg acc ttc atg tct ggg gag gtg ggg cgc	882
Val Glu Thr Leu Arg Tyr Leu Thr Phe Met Ser Gly Glu Val Gly Arg	
250 255 260	
atc aca aag tgg aag tac ccg ttc ccc aag gag aca gag gcc aag agc	930
Ile Thr Lys Trp Lys Tyr Pro Phe Pro Lys Glu Thr Glu Ala Lys Ser	
265 270 275	
aag ctg acg ccc act ctg tat gtt ggg aaa tac tct acc agc ctc tat	978
Lys Leu Thr Pro Thr Leu Tyr Val Gly Lys Tyr Ser Thr Ser Leu Tyr	
280 285 290	
gcc tct ccc tca atg gta cac gag ggg gtt gct gtc gtg ccc cgc ggc	1026
Ala Ser Pro Ser Met Val His Glu Gly Val Ala Val Val Pro Arg Gly	
295 300 305 310	
agc aca ctt cct ttg ctg gaa ggg ccc cag act gat ggc gtc acc atc	1074
Ser Thr Leu Pro Leu Leu Glu Gly Pro Gln Thr Asp Gly Val Thr Ile	
315 320 325	
ggg gac aag ggg gag tgt gtg atc acg ccc agc acg gac gtc aag ttt	1122
Gly Asp Lys Gly Glu Cys Val Ile Thr Pro Ser Thr Asp Val Lys Phe	
330 335 340	
gat ccc gga ctc aaa agc aag aac aag ctc aac tac ttg agg aat tac	1170
Asp Pro Gly Leu Lys Ser Lys Asn Lys Leu Asn Tyr Leu Arg Asn Tyr	

345	350	355	
tgg ctt ctg ata gga cac cat gaa acc cca ctg tct gcg tct acc aag			1218
Trp Leu Leu Ile Gly His His Glu Thr Pro Leu Ser Ala Ser Thr Lys			
360	365	370	
atg ctg gag aga ttt ccc aac aat cta ccc aaa cat cgg gaa aat gtg			1266
Met Leu Glu Arg Phe Pro Asn Asn Leu Pro Lys His Arg Glu Asn Val			
375	380	385	390
att cct gct gat tca gag aaa aag agc ttt gag gaa gtt atc aac ctg			1314
Ile Pro Ala Asp Ser Glu Lys Lys Ser Phe Glu Glu Val Ile Asn Leu			
	395	400	405
gtt gac cag act tca gaa aac gca cct acc acc gtg tct cgg gat gtg			1362
Val Asp Gln Thr Ser Glu Asn Ala Pro Thr Thr Val Ser Arg Asp Val			
	410	415	420
gag gag aag ccc gcc cat gcc cct gcc cgg ccc gag gcc ccc gtg gac			1410
Glu Glu Lys Pro Ala His Ala Pro Ala Arg Pro Glu Ala Pro Val Asp			
	425	430	435
tcc atg ctt aag gac atg gct acc atc atc ctg agc acc ttc ctg ctg			1458
Ser Met Leu Lys Asp Met Ala Thr Ile Ile Leu Ser Thr Phe Leu Leu			
	440	445	450
att ggc tgg gtg gcc ttc atc atc acc tat ccc ctg agc atg cat cag			1506
Ile Gly Trp Val Ala Phe Ile Ile Thr Tyr Pro Leu Ser Met His Gln			
	455	460	465
cag cag cag ctc cag cac cag cag ttc cag aag gaa ctg gag aag atc			1554
Gln Gln Gln Leu Gln His Gln Gln Phe Gln Lys Glu Leu Glu Lys Ile			
	475	480	485
cag ctc ctg cag cag cag cag cag cag ctg ccc ttc cac cca cct gga			1602
Gln Leu Leu Gln Gln Gln Gln Gln Gln Leu Pro Phe His Pro Pro Gly			
	490	495	500
gac acg gct cag gac ggc gag ctc ctg gac acg tct ggc ccg tac tca			1650
Asp Thr Ala Gln Asp Gly Glu Leu Leu Asp Thr Ser Gly Pro Tyr Ser			
	505	510	515
gag agc tcg ggc acc agc agc ccc agc acg tcc ccc agg gcc tcc aac			1698
Glu Ser Ser Gly Thr Ser Ser Pro Ser Thr Ser Pro Arg Ala Ser Asn			
	520	525	530
cac tcg ctc tgc tcc ggc agc tct gcc tcc aag gct ggc agc agc ccc			1746
His Ser Leu Cys Ser Gly Ser Ser Ala Ser Lys Ala Gly Ser Ser Pro			
	535	540	545
tcc ctg gaa caa gac gat gga gat gag gaa acc agc gtg gtg ata gtt			1794
Ser Leu Glu Gln Asp Asp Gly Asp Glu Glu Thr Ser Val Val Ile Val			
	555	560	565
ggg aaa att tcc ttc tgt ccc aag gat gtc ctg ggc cat gga gct gag			1842
Gly Lys Ile Ser Phe Cys Pro Lys Asp Val Leu Gly His Gly Ala Glu			
	570	575	580
ggc aca att gtg tac cgg ggc atg ttt gac aac cgc gac gtg gcc gtg			1890
Gly Thr Ile Val Tyr Arg Gly Met Phe Asp Asn Arg Asp Val Ala Val			
	585	590	595

aag agg atc ctc ccc gag tgt ttt agc ttc gca gac cgt gag gtc cag Lys Arg Ile Leu Pro Glu Cys Phe Ser Phe Ala Asp Arg Glu Val Gln 600 605 610	1938
ctg ttg cga gaa tcg gat gag cac ccg aac gtg atc cgc tac ttc tgc Leu Leu Arg Glu Ser Asp Glu His Pro Asn Val Ile Arg Tyr Phe Cys 615 620 625 630	1986
acg gag aag gac cgg caa ttc cag tac att gcc atc gag ctg tgt gca Thr Glu Lys Asp Arg Gln Phe Gln Tyr Ile Ala Ile Glu Leu Cys Ala 635 640 645	2034
gcc acc ctg caa gag tat gtg gag cag aag gac ttt gcg cat ctc ggc Ala Thr Leu Gln Glu Tyr Val Glu Gln Lys Asp Phe Ala His Leu Gly 650 655 660	2082
ctg gag ccc atc acc ttg ctg cag cag acc acc tcg ggc ctg gcc cac Leu Glu Pro Ile Thr Leu Leu Gln Gln Thr Thr Ser Gly Leu Ala His 665 670 675	2130
ctc cac tcc ctc aac atc gtt cac aga gac cta aag cca cac aac atc Leu His Ser Leu Asn Ile Val His Arg Asp Leu Lys Pro His Asn Ile 680 685 690	2178
ctc ata tcc atg ccc aat gca cac ggc aag atc aag gcc atg atc tcc Leu Ile Ser Met Pro Asn Ala His Gly Lys Ile Lys Ala Met Ile Ser 695 700 705 710	2226
gac ttt ggc ctc tgc aag aag ctg gca gtg ggc aga cac agt ttc agc Asp Phe Gly Leu Cys Lys Lys Leu Ala Val Gly Arg His Ser Phe Ser 715 720 725	2274
cgc cga tct ggg gtg cct ggc aca gaa ggc tgg atc gct cca gag atg Arg Arg Ser Gly Val Pro Gly Thr Glu Gly Trp Ile Ala Pro Glu Met 730 735 740	2322
ctg agc gaa gac tgt aag gag aac cct acc tac acg gtg gac atc ttt Leu Ser Glu Asp Cys Lys Glu Asn Pro Thr Tyr Thr Val Asp Ile Phe 745 750 755	2370
tct gca ggc tgc gtc ttt tac tac gtg gtc tct gag ggc agc cac cct Ser Ala Gly Cys Val Phe Tyr Tyr Val Val Ser Glu Gly Ser His Pro 760 765 770	2418
ttt ggc aag tcc ctg cag cgg cag gcc aac atc ctc ctg ggt gcc tgc Phe Gly Lys Ser Leu Gln Arg Gln Ala Asn Ile Leu Leu Gly Ala Cys 775 780 785 790	2466
agc ctt gac tgc ttg cac cca gag aag cac gaa gac gtc att gca cga Ser Leu Asp Cys Leu His Pro Glu Lys His Glu Asp Val Ile Ala Arg 795 800 805	2514
gaa ttg ata gag aag atg att gcg atg gat cct cag aaa cgc ccc tca Glu Leu Ile Glu Lys Met Ile Ala Met Asp Pro Gln Lys Arg Pro Ser 810 815 820	2562
gcg aac gac gtg ctc aaa cac ccg ttc ttc tgg agc cta gag aag cag Ala Asn Asp Val Leu Lys His Pro Phe Phe Trp Ser Leu Glu Lys Gln 825 830 835	2610

ctc cag ttc ttc cag gac gtg agc gac aga ata gaa aag gaa tcc ctg 2658
Leu Gln Phe Phe Gln Asp Val Ser Asp Arg Ile Glu Lys Glu Ser Leu
840 845 850

gat ggc ccg atc gtg aag cag tta gag aga ggc ggg aga gcc gtg gtg 2706
Asp Gly Pro Ile Val Lys Gln Leu Glu Arg Gly Gly Arg Ala Val Val
855 860 865 870

aag atg gac tgg cgg gag aac atc act gac ccc ctc cag aca gac ctg 2754
Lys Met Asp Trp Arg Glu Asn Ile Thr Asp Pro Leu Gln Thr Asp Leu
875 880 885

cgt aaa ttc agg acc tat aaa ggt ggt tct gtc aga gat ctc ctc cga 2802
Arg Lys Phe Arg Thr Tyr Lys Gly Gly Ser Val Arg Asp Leu Leu Arg
890 895 900

gcc atg aga aat aag aag cac cac tac cgg gag ctg cct gca gag gtg 2850
Ala Met Arg Asn Lys Lys His His Tyr Arg Glu Leu Pro Ala Glu Val
905 910 915

cgg gag acg ctg ggg acc ctc ccc gac gac ttc gtg tgc tac ttc acg 2898
Arg Glu Thr Leu Gly Thr Leu Pro Asp Asp Phe Val Cys Tyr Phe Thr
920 925 930

tct cgc ttc ccc cac ctc ctc gca cac acc tac cgg gcc atg gag ctg 2946
Ser Arg Phe Pro His Leu Leu Ala His Thr Tyr Arg Ala Met Glu Leu
935 940 945 950

tgc agc cac gag aga ctc ttc cag ccc tac tac ttc cac gag ccc cca 2994
Cys Ser His Glu Arg Leu Phe Gln Pro Tyr Tyr Phe His Glu Pro Pro
955 960 965

gag ccc cag ccc cca gtg act cca gac gcc ctc tgagcagagg cgccccctct 3047
Glu Pro Gln Pro Pro Val Thr Pro Asp Ala Leu
970 975

gttctggttg cccagctgt gactgagggc ctggtcacca caattagagc ttgatgcctc 3107

ccggctttgc agggagacca ggcttcccaa accaagtgcc ttgagctgcc tgctctgcag 3167

cccacagagg acagtgctga cccaggaag tgggagaagt ggccccctgt gacctacagg 3227

gaactgggaa gatgctggcc ccaaaagcct tacgggtcatg atgtctgcaa aggagggcct 3287

cagagacagc gcgagtagca cccccagcca tctactggat aaacttgctt cagacttttt 3347

aaattcctgc ttaatgtcag tctacaggcc tttcaggaag ggagaggagg gaatcgtaca 3407

ttttgcttgc gtgctgggac agctaggctg agatgcacca agtacagcct tctactggaga 3467

ccggaattga gaggtggggg atgctgagga gggggaggac ggagttcaga ggggtgtcgtc 3527

ctgcagtatg agattttctca ttgatcacag atgtgccag agtagcccag gtcactgtta 3587

actagtgttt ctgcagaggc agcaggagcc agcccgaat tc 3629

<210> 2

<211> 977

<212> PRT

<213> Homo sapiens

<400> 2

Met Pro Ala Arg Arg Leu Leu Leu Leu Leu Thr Leu Leu Leu Pro Gly
 1 5 10 15
 Leu Gly Ile Phe Gly Ser Thr Ser Thr Val Thr Leu Pro Glu Thr Leu
 20 25 30
 Leu Phe Val Ser Thr Leu Asp Gly Ser Leu His Ala Val Ser Lys Arg
 35 40 45
 Thr Gly Ser Ile Lys Trp Thr Leu Lys Glu Asp Pro Val Leu Gln Val
 50 55 60
 Pro Thr His Val Glu Glu Pro Ala Phe Leu Pro Asp Pro Asn Asp Gly
 65 70 75 80
 Ser Leu Tyr Thr Leu Gly Ser Lys Asn Asn Glu Gly Leu Thr Lys Leu
 85 90 95
 Pro Phe Thr Ile Pro Glu Leu Val Gln Ala Ser Pro Cys Arg Ser Ser
 100 105 110
 Asp Gly Ile Leu Tyr Met Gly Lys Lys Gln Asp Ile Trp Tyr Val Ile
 115 120 125
 Asp Leu Leu Thr Gly Glu Lys Gln Gln Thr Leu Ser Ser Ala Phe Ala
 130 135 140
 Asp Ser Leu Cys Pro Ser Thr Ser Leu Leu Tyr Leu Gly Arg Thr Glu
 145 150 155 160
 Tyr Thr Ile Thr Met Tyr Asp Thr Lys Thr Arg Glu Leu Arg Trp Asn
 165 170 175
 Ala Thr Tyr Phe Asp Tyr Ala Ala Ser Leu Pro Glu Asp Glu Gly Asp
 180 185 190
 Tyr Lys Met Ser His Phe Val Ser Asn Gly Asp Gly Leu Val Val Thr
 195 200 205
 Val Asp Ser Glu Ser Gly Asp Val Leu Trp Ile Gln Asn Tyr Ala Ser
 210 215 220
 Pro Val Val Ala Phe Tyr Val Trp Gln Arg Glu Gly Leu Arg Lys Val
 225 230 235 240
 Met His Ile Asn Val Ala Val Glu Thr Leu Arg Tyr Leu Thr Phe Met
 245 250 255
 Ser Gly Glu Val Gly Arg Ile Thr Lys Trp Lys Tyr Pro Phe Pro Lys
 260 265 270
 Glu Thr Glu Ala Lys Ser Lys Leu Thr Pro Thr Leu Tyr Val Gly Lys
 275 280 285
 Tyr Ser Thr Ser Leu Tyr Ala Ser Pro Ser Met Val His Glu Gly Val
 290 295 300
 Ala Val Val Pro Arg Gly Ser Thr Leu Pro Leu Leu Glu Gly Pro Gln

305		310		315		320
Thr Asp Gly Val	Thr Ile Gly Asp Lys	Gly Glu Cys Val	Ile Thr Pro			
	325		330			335
Ser Thr Asp Val	Lys Phe Asp Pro Gly	Leu Lys Ser Lys	Asn Lys Leu			
	340		345			350
Asn Tyr Leu Arg	Asn Tyr Trp Leu Leu	Ile Gly His His	Glu Thr Pro			
	355		360			365
Leu Ser Ala Ser	Thr Lys Met Leu Glu	Arg Phe Pro Asn	Asn Leu Pro			
	370		375			380
Lys His Arg Glu	Asn Val Ile Pro Ala	Asp Ser Glu Lys	Lys Ser Phe			
	385		390			395
Glu Glu Val Ile	Asn Leu Val Asp Gln	Thr Ser Glu Asn	Ala Pro Thr			
	405		410			415
Thr Val Ser Arg	Asp Val Glu Glu Lys	Pro Ala His Ala	Pro Ala Arg			
	420		425			430
Pro Glu Ala Pro	Val Asp Ser Met Leu	Lys Asp Met Ala	Thr Ile Ile			
	435		440			445
Leu Ser Thr Phe	Leu Leu Ile Gly Trp	Val Ala Phe Ile	Ile Thr Tyr			
	450		455			460
Pro Leu Ser Met	His Gln Gln Gln Gln	Leu Gln His Gln	Gln Phe Gln			
	465		470			475
Lys Glu Leu Glu	Lys Ile Gln Leu Leu	Gln Gln Gln Gln	Gln Gln Leu			
	485		490			495
Pro Phe His Pro	Pro Gly Asp Thr Ala	Gln Asp Gly Glu	Leu Leu Asp			
	500		505			510
Thr Ser Gly Pro	Tyr Ser Glu Ser Ser	Gly Thr Ser Ser	Pro Ser Thr			
	515		520			525
Ser Pro Arg Ala	Ser Asn His Ser Leu	Cys Ser Gly Ser	Ser Ala Ser			
	530		535			540
Lys Ala Gly Ser	Ser Pro Ser Leu Glu	Gln Asp Asp Gly	Asp Glu Glu			
	545		550			555
Thr Ser Val Val	Ile Val Gly Lys Ile	Ser Phe Cys Pro	Lys Asp Val			
	565		570			575
Leu Gly His Gly	Ala Glu Gly Thr Ile	Val Tyr Arg Gly	Met Phe Asp			
	580		585			590
Asn Arg Asp Val	Ala Val Lys Arg Ile	Leu Pro Glu Cys	Phe Ser Phe			
	595		600			605
Ala Asp Arg Glu	Val Gln Leu Leu Arg	Glu Ser Asp Glu	His Pro Asn			
	610		615			620
Val Ile Arg Tyr	Phe Cys Thr Glu Lys	Asp Arg Gln Phe	Gln Tyr Ile			
	625		630			635
						640

Ala Ile Glu Leu Cys Ala Ala Thr Leu Gln Glu Tyr Val Glu Gln Lys
 645 650 655
 Asp Phe Ala His Leu Gly Leu Glu Pro Ile Thr Leu Leu Gln Gln Thr
 660 665 670
 Thr Ser Gly Leu Ala His Leu His Ser Leu Asn Ile Val His Arg Asp
 675 680 685
 Leu Lys Pro His Asn Ile Leu Ile Ser Met Pro Asn Ala His Gly Lys
 690 695 700
 Ile Lys Ala Met Ile Ser Asp Phe Gly Leu Cys Lys Lys Leu Ala Val
 705 710 715 720
 Gly Arg His Ser Phe Ser Arg Arg Ser Gly Val Pro Gly Thr Glu Gly
 725 730 735
 Trp Ile Ala Pro Glu Met Leu Ser Glu Asp Cys Lys Glu Asn Pro Thr
 740 745 750
 Tyr Thr Val Asp Ile Phe Ser Ala Gly Cys Val Phe Tyr Tyr Val Val
 755 760 765
 Ser Glu Gly Ser His Pro Phe Gly Lys Ser Leu Gln Arg Gln Ala Asn
 770 775 780
 Ile Leu Leu Gly Ala Cys Ser Leu Asp Cys Leu His Pro Glu Lys His
 785 790 795 800
 Glu Asp Val Ile Ala Arg Glu Leu Ile Glu Lys Met Ile Ala Met Asp
 805 810 815
 Pro Gln Lys Arg Pro Ser Ala Asn Asp Val Leu Lys His Pro Phe Phe
 820 825 830
 Trp Ser Leu Glu Lys Gln Leu Gln Phe Phe Gln Asp Val Ser Asp Arg
 835 840 845
 Ile Glu Lys Glu Ser Leu Asp Gly Pro Ile Val Lys Gln Leu Glu Arg
 850 855 860
 Gly Gly Arg Ala Val Val Lys Met Asp Trp Arg Glu Asn Ile Thr Asp
 865 870 875 880
 Pro Leu Gln Thr Asp Leu Arg Lys Phe Arg Thr Tyr Lys Gly Gly Ser
 885 890 895
 Val Arg Asp Leu Leu Arg Ala Met Arg Asn Lys Lys His His Tyr Arg
 900 905 910
 Glu Leu Pro Ala Glu Val Arg Glu Thr Leu Gly Thr Leu Pro Asp Asp
 915 920 925
 Phe Val Cys Tyr Phe Thr Ser Arg Phe Pro His Leu Leu Ala His Thr
 930 935 940
 Tyr Arg Ala Met Glu Leu Cys Ser His Glu Arg Leu Phe Gln Pro Tyr
 945 950 955 960

Tyr Phe His Glu Pro Pro Glu Pro Gln Pro Pro Val Thr Pro Asp Ala
965 970 975

Leu

<210> 3

<211> 983

<212> PRT

<213> Caenorhabditis elegans

<400> 3

Met Arg Ala Thr Phe His Leu Phe Thr Phe Ile Phe Leu Leu Leu Phe
1 5 10 15

Ser Ser Val Ile Cys Ile Ser Thr Pro Gly Phe Arg Asn Asp His Glu
20 25 30

Ser Ile Gly Asp Asp Glu Glu Lys Thr Ser Ser Thr Ile Leu Val Ser
35 40 45

Thr Ile Asp Gly Arg Leu Arg Ala Leu Asp Ser Glu Thr Gly Glu Ile
50 55 60

Lys Trp Thr Leu Gln Glu Glu Pro Val Leu Arg Ser Pro Ser Ala Val
65 70 75 80

Lys Gln Gly Phe Thr Phe Leu Pro Asn Pro Leu Asp Gly Ser Leu Tyr
85 90 95

Val Leu Lys Asn Ser Ser Leu Lys Lys Leu Pro Phe Asn Ile Pro Gln
100 105 110

Leu Val His Ala Ser Pro Cys Lys Gly Asn Asp Gly Ile Leu Tyr Ala
115 120 125

Gly Ser Lys Lys Asp Val Trp Phe Gly Ile Asp Pro Lys Thr Gly Leu
130 135 140

Lys Val Glu Tyr Ile Leu Leu Asn Ile Ser Asp Lys Ile Leu Phe Leu
145 150 155 160

Gln Val Glu Thr Leu Ser Ser Ala Ser Ala Asp Arg Ile Cys Pro Ala
165 170 175

Asn Gln Lys Gln Thr Ile Phe Leu Gly Arg Thr Glu Tyr Arg Val Ser
180 185 190

Met Phe Asp Glu Lys Asn Arg Gly Lys Thr Trp Asn Ala Thr Phe Asn
195 200 205

Asp Tyr Ser Ala His Leu Leu Pro Glu Val Asn Thr Trp Pro Phe Lys
210 215 220

His Tyr Ala Ser Ser Ser His Gly Tyr Ile Leu Thr Phe Asp Arg Glu
225 230 235 240

Thr Gly Glu Met Arg Trp Glu Gln Asp Leu Lys Gln Pro Val Val Ala
245 250 255

Leu Tyr Leu Leu Arg Asp Asp Gly Leu His Lys Leu Pro Phe Glu Val
 260 265 270
 Met Gly Lys Glu Thr Met Glu Asn Val Ala Lys Asn Ile Phe Thr Val
 275 280 285
 Asp Gln Trp Pro Thr Val Leu Gly Val Asn Ala Ala Asp Pro Gln Thr
 290 295 300
 Thr Ser Leu Thr Asn Gln Phe Phe Pro Ala Leu Phe Val Gly Glu Ser
 305 310 315 320
 Ser Phe Gly Leu Tyr Ala Ile Glu Ala Leu Val Asp His Gln Thr Ile
 325 330 335
 Thr Tyr Ser Pro Lys Leu Leu Gly Pro Pro Leu Leu Glu Gly Pro Ala
 340 345 350
 Pro Ile Ala Leu Thr Glu Met Glu Lys Glu Glu Tyr Leu Pro Pro Arg
 355 360 365
 Arg Pro Ile Ile Arg Asn Ile Pro Pro Ser Ile Thr His Lys Thr Ser
 370 375 380
 Asp Gly Glu Tyr Leu Leu Leu Gly Tyr His Asp Arg Pro Met Met Thr
 385 390 395 400
 Met Ala Thr Ile Ile Pro Thr Arg Tyr Pro Val Pro Gly Pro His Lys
 405 410 415
 Ala Ile Gly Ser Thr Ile Glu Arg Pro Pro Pro Gln Leu Leu Gly Pro
 420 425 430
 Val Glu Pro Gln Lys His Glu Asp Thr Ser Phe Ile Leu Leu Leu Leu
 435 440 445
 Asn Asn His Pro Ile Pro Phe Tyr Ala Thr Leu Val Thr Met Phe Ala
 450 455 460
 Leu Leu Leu Thr Val Ile Trp Gln Cys Gly Arg Gln Trp Asp Gln Gln
 465 470 475 480
 Lys Ser Thr Ser Arg Met Asp Ser Phe Glu Ile Val Asn Asn Pro Gly
 485 490 495
 Glu Ser Arg Ser Ala Gln Thr Ser Lys Gln Ser Asn Arg Gly Ser Phe
 500 505 510
 Gly Trp Ala Asn Arg Lys Ile Glu Ile Pro Glu Gly Trp Met Ala Val
 515 520 525
 Gly Ser Lys Leu Met Tyr Ser Pro Ser Asp Ile Leu Gly Thr Gly Cys
 530 535 540
 Glu Gly Thr Val Val Tyr Arg Gly Thr Phe Asp Gly Arg Glu Val Ala
 545 550 555 560
 Val Lys Arg Val Val Ser Glu Phe Val Lys Phe Ala His Arg Glu Ala
 565 570 575
 Asp Leu Leu Arg Glu Ser Asp Thr His Pro His Val Ile Arg Tyr Phe

580					585					590					
Cys	Met	Glu	Ser	Asp	Ser	Gln	Phe	Arg	Tyr	Leu	Ala	Leu	Glu	Leu	Cys
		595					600					605			
Ile	Ala	Ser	Leu	Asn	Asp	Tyr	Val	Glu	Gln	Lys	Glu	Val	Gln	Gln	Asn
	610					615					620				
Val	Thr	Ile	Ala	Leu	Arg	Asp	Ile	Met	Lys	Gln	Ala	Thr	Asp	Gly	Leu
625					630					635					640
Ala	His	Leu	His	Ala	Ser	Lys	Ile	Val	His	Arg	Asp	Met	Lys	Pro	Gln
				645					650					655	
Asn	Val	Leu	Ile	Thr	Met	Ala	Ser	Gln	Arg	Gly	Glu	Met	Arg	Ala	Val
			660					665					670		
Ile	Ser	Asp	Phe	Gly	Leu	Cys	Lys	Arg	Val	Gln	Pro	Gly	Lys	Asn	Ser
		675					680					685			
Ile	Ser	Arg	Gly	Ile	Ala	Ser	Gly	Leu	Ala	Gly	Thr	Asp	Gly	Trp	Ile
	690					695					700				
Ala	Pro	Glu	Val	Leu	Ile	Ser	Ala	Ser	Thr	Ser	Tyr	Pro	Val	Asp	Ile
705					710						715				720
Phe	Ser	Leu	Gly	Cys	Ile	Phe	Tyr	Tyr	Val	Leu	Thr	Ser	Gly	Thr	His
				725					730					735	
Pro	Phe	Gly	Lys	Ser	Leu	His	Arg	Gln	Ala	Asn	Ile	Val	Asn	Gly	Glu
			740					745					750		
Tyr	Thr	Leu	Asn	Lys	Leu	Ala	Asp	Leu	Asp	Asp	Trp	Ser	Leu	Ala	Asp
		755					760					765			
Asp	Leu	Ile	Ser	Ser	Met	Leu	Asn	Val	Glu	Pro	Leu	His	Arg	Leu	Thr
	770					775					780				
Ala	Asp	Ala	Val	Leu	Asn	His	Pro	Phe	Phe	Trp	Thr	Ser	Glu	Lys	Arg
785					790					795					800
Leu	Ala	Tyr	Phe	Ser	Asp	Val	Ser	Asp	Arg	Val	Glu	Lys	Glu	Glu	Asp
				805					810					815	
Asn	Ser	Pro	Val	Val	Arg	Arg	Ile	Glu	Thr	Asp	Ala	Arg	Ile	Val	Val
			820					825					830		
Cys	Gly	Gly	Trp	Arg	Glu	Lys	Ile	Cys	Asp	Ala	Leu	Lys	Glu	Asp	Leu
		835					840					845			
Arg	Lys	Phe	Arg	Thr	Tyr	Lys	Ser	Phe	Ser	Val	Arg	Asp	Leu	Leu	Arg
	850					855					860				
Ala	Met	Arg	Asn	Lys	Lys	His	His	Tyr	Arg	Glu	Leu	Pro	Glu	Asp	Val
865					870					875					880
Arg	Gln	Ser	Leu	Gly	Asp	Ile	Pro	Asp	Gln	Phe	Leu	His	Tyr	Phe	Thr
				885					890					895	
Ser	Arg	Phe	Pro	Arg	Leu	Leu	Leu	His	Val	Tyr	Lys	Ala	Thr	Glu	Tyr
			900					905					910		

Cys Ser Gly Glu Ala Val Phe Lys Arg Tyr Tyr Ser Asp Asp Val Arg
915 920 925

Ala Arg Met Tyr Pro Ile Val Glu Glu Glu Glu Arg Val Arg Lys Lys
930 935 940

Ile Lys Glu Glu Met Ala Asn Glu Val Trp Ala Arg Ala Pro Lys Pro
945 950 955 960

Val Glu Gln Arg Thr Pro Leu Lys Leu Asp Lys Arg Asn Ile Lys Lys
965 970 975

Lys Ser Asn Pro Asn Thr Asp
980

<210> 4

<211> 443

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 4

Leu Val Val Ser Cys Lys Ile Leu Gly Tyr Gly Ser Ser Gly Thr Val
1 5 10 15

Val Phe Gln Gly Ser Phe Gln Gly Arg Pro Val Ala Val Lys Arg Met
20 25 30

Leu Ile Asp Phe Cys Asp Ile Ala Leu Met Glu Ile Lys Leu Leu Thr
35 40 45

Glu Ser Asp Asp His Pro Asn Val Ile Arg Tyr Tyr Cys Ser Glu Thr
50 55 60

Thr Asp Arg Phe Leu Tyr Ile Ala Leu Glu Leu Cys Asn Leu Asn Leu
65 70 75 80

Gln Asp Leu Val Glu Ser Lys Asn Val Ser Asp Glu Asn Leu Lys Leu
85 90 95

Gln Lys Glu Tyr Asn Pro Ile Ser Leu Leu Arg Gln Ile Ala Ser Gly
100 105 110

Val Ala His Leu His Ser Leu Lys Ile Ile His Arg Asp Leu Lys Pro
115 120 125

Gln Asn Ile Leu Val Ser Thr Ser Ser Arg Phe Thr Ala Asp Gln Gln
130 135 140

Thr Gly Ala Glu Asn Leu Arg Ile Leu Ile Ser Asp Phe Gly Leu Cys
145 150 155 160

Lys Lys Leu Asp Ser Gly Gln Ser Ser Phe Arg Thr Asn Leu Asn Asn
165 170 175

Pro Ser Gly Thr Ser Gly Trp Arg Ala Pro Glu Leu Leu Glu Glu Ser
180 185 190

Asn Asn Leu Gln Cys Gln Val Glu Thr Glu His Ser Ser Ser Arg His
195 200 205

Thr Val Val Ser Ser Asp Ser Phe Tyr Asp Pro Phe Thr Lys Arg Arg
 210 215 220

Leu Thr Arg Ser Ile Asp Ile Phe Ser Met Gly Cys Val Phe Tyr Tyr
 225 230 235 240

Ile Leu Ser Lys Gly Lys His Pro Phe Gly Asp Lys Tyr Ser Arg Glu
 245 250 255

Ser Asn Ile Ile Arg Gly Ile Phe Ser Leu Asp Glu Met Lys Cys Leu
 260 265 270

His Asp Arg Ser Leu Ile Ala Glu Ala Thr Asp Leu Ile Ser Gln Met
 275 280 285

Ile Asp His Asp Pro Leu Lys Arg Pro Thr Ala Met Lys Val Leu Arg
 290 295 300

His Pro Leu Phe Trp Pro Lys Ser Lys Lys Leu Glu Phe Leu Leu Lys
 305 310 315 320

Val Ser Asp Arg Leu Glu Ile Glu Asn Arg Asp Pro Pro Ser Ala Leu
 325 330 335

Leu Met Lys Phe Asp Ala Gly Ser Asp Phe Val Ile Pro Ser Gly Asp
 340 345 350

Trp Thr Val Lys Phe Asp Lys Thr Phe Met Asp Asn Leu Glu Arg Tyr
 355 360 365

Arg Lys Tyr His Ser Ser Lys Leu Met Asp Leu Leu Arg Ala Leu Arg
 370 375 380

Asn Lys Tyr His His Phe Met Asp Leu Pro Glu Asp Ile Ala Glu Leu
 385 390 395 400

Met Gly Pro Val Pro Asp Gly Phe Tyr Asp Tyr Phe Thr Lys Arg Phe
 405 410 415

Pro Asn Leu Leu Ile Gly Val Tyr Met Ile Val Lys Glu Asn Leu Ser
 420 425 430

Asp Asp Gln Ile Leu Arg Glu Phe Leu Tyr Ser
 435 440

<210> 5

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 5

Ile Ser Asp Phe Gly Leu Cys Lys
 1 5

<210> 6

<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 6
cgccatgcc

9

<210> 7
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_feature
<222> 1
<223> N may be Thymine or Cytosine

<220>
<221> misc_feature
<222> 4,9,13,16
<223> N may be Adenine or Guanine

<220>
<221> misc_feature
<222> 7,10,19,22
<223> N may be any nucleotide

<220>
<221> misc_feature
<222> 21
<223> N may be Adenine or Thymine

<220>
<223> Description of Artificial Sequence: Primer

<400> 7
nttncntntnn ccnaantcng nnat

24

<210> 8
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 8
Ile Ser Asp Phe Gly Leu Cys Lys
1 5

<210> 9
<211> 28
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 9

gctctagaac catgccggcc cggcggt

28

<210> 10

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 10

aggctgccat cattaggatc t

21

<210> 11

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 11

cattgatgtg catcaccttc ctc

23

<210> 12

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 12

cggaattcat cacctatccc ctgagcatg

29

<210> 13

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 13

cggaattctc agagggcgtc tggagtca

28